

#6

OIEP

RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/656,309

TIME: 11:25:44

Input Set : A:\es.txt

Output Set: N:\CRF3\04162001\I656309.raw

ENTERED

3 <110> APPLICANT: DIVERSA CORPORATION
 4 CALLEN, Walter
 5 MATHUR, Eric
 7 <120> TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND
 METHODS OF USE
 8 THEREOF
 10 <130> FILE REFERENCE: DIVER1350-2
 12 <140> CURRENT APPLICATION NUMBER: US 09/656,309
 13 <141> CURRENT FILING DATE: 2000-09-06
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2412
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Pyrolobus fumarius
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(2412)
 28 <400> SEQUENCE: 1
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 30 Met Thr Glu Val Val Phe Thr Val Leu Asp Ser Ser Tyr Glu Val Val
 31 1 5 10 15
 33 ggt aaa gag cct cag gta atc ata tgg ggt att gct gag aac ggc gag 96
 34 Gly Lys Glu Pro Gln Val Ile Ile Trp Gly Ile Ala Glu Asn Gly Glu
 35 20 25 30
 37 agg gta gtc ctc att gac agg tct ttt cgc cca tac ttc tat gcg ctg 144
 38 Arg Val Val Leu Ile Asp Arg Ser Phe Arg Pro Tyr Phe Tyr Ala Leu
 39 35 40 45
 41 ctt gca ccg ggc gcc gat cct aag cag gta gca caa cgt att cgt gca 192
 42 Leu Ala Pro Gly Ala Asp Pro Lys Gln Val Ala Gln Arg Ile Arg Ala
 43 50 55 60
 45 ttg agt agg cca aag agc ccg att ata ggt gta gag gat gac aag agg 240
 46 Leu Ser Arg Pro Lys Ser Pro Ile Ile Gly Val Glu Asp Asp Lys Arg
 47 65 70 75 80
 49 aag tac ttc ggg agg cct cgt agg gtc tta cgt att cgc acc gtg cta 288
 50 Lys Tyr Phe Gly Arg Pro Arg Arg Val Leu Arg Ile Arg Thr Val Leu
 51 85 90 95
 53 ccc gag gct gtt agg gag tat cgc gaa ctc gta aag aac gtt gat ggt 336
 54 Pro Glu Ala Val Arg Glu Tyr Arg Glu Leu Val Lys Asn Val Asp Gly
 55 100 105 110
 57 gtt gag gat gtt cta gag gcg gat ata cgc ttc gct atg cgc tat ctc 384
 58 Val Glu Asp Val Leu Glu Ala Asp Ile Arg Phe Ala Met Arg Tyr Leu
 59 115 120 125
 61 ata gat cac gat cta ttt cct ttc acc tgg tac cgt gta gag gct gag 432
 62 Ile Asp His Asp Leu Phe Pro Phe Thr Trp Tyr Arg Val Glu Ala Glu
 63 130 135 140
 65 ccg ctc gag aac aag atg ggc ttc cgt gtc gac aag gta tac ctg gtt 480
 66 Pro Leu Glu Asn Lys Met Gly Phe Arg Val Asp Lys Val Tyr Leu Val

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67	145		150		155		160	
69	aag agc agg ccg gag cca ctt tat ggt gag gct ctc gca cca acc aag						528	
70	Lys Ser Arg Pro Glu Pro Leu Tyr Gly Glu Ala Leu Ala Pro Thr Lys							
71		165		170		175		
73	ctt ccc gat ctt agg ata ctc gcg ttc gat att gaa gtt tat agc aag					576		
74	Leu Pro Asp Leu Arg Ile Leu Ala Phe Asp Ile Glu Val Tyr Ser Lys							
75		180		185		190		
77	caa ggg tcg ccg cgt cca gag cgc gat cct gta ata gtg ata gct gtg					624		
78	Gln Gly Ser Pro Arg Pro Glu Arg Asp Pro Val Ile Val Ile Ala Val							
79		195		200		205		
81	aag act gac gat ggc gat gag gtg cta ttc att gca gag ggc aaa gac					672		
82	Lys Thr Asp Asp Gly Asp Glu Val Leu Phe Ile Ala Glu Gly Lys Asp							
83		210		215		220		
85	gat cga aaa ccg ata cgc gag ttt gta gag tac gtg aag agg tat gac					720		
86	Asp Arg Lys Pro Ile Arg Glu Phe Val Glu Tyr Val Lys Arg Tyr Asp							
87	225		230		235	240		
89	ccc gac ata ata gtc ggt tat aac aac aat cat ttc gat tgg cct tat					768		
90	Pro Asp Ile Ile Val Gly Tyr Asn Asn Asn His Phe Asp Trp Pro Tyr							
91		245		250		255		
93	ctt ttg agg cgc gcc cgc atc cta ggc ata aag ctt gat gtg act aga					816		
94	Leu Leu Arg Arg Ala Arg Ile Leu Gly Ile Lys Leu Asp Val Thr Arg							
95		260		265		270		
97	aga gtt ggc gcc gag ccc acc act agc gta cat ggg cac gtc tct gtc					864		
98	Arg Val Gly Ala Glu Pro Thr Thr Ser Val His Gly His Val Ser Val							
99		275		280		285		
101	cct ggc agg ctt aac gta gat ctg tac gac tat gcc gaa gag atg cca					912		
102	Pro Gly Arg Leu Asn Val Asp Leu Tyr Asp Tyr Ala Glu Glu Met Pro							
103		290		295		300		
105	gag atc aag ata aag agt ctc gag gag gtc gca gag tat cta ggc gtg					960		
106	Glu Ile Lys Ile Lys Ser Leu Glu Glu Val Ala Glu Tyr Leu Gly Val							
107	305		310		315	320		
109	atg aag aag agt gaa cgc gtt atc atc aat tgg tgg gag att cca gac					1008		
110	Met Lys Lys Ser Glu Arg Val Ile Ile Asn Trp Trp Glu Ile Pro Asp							
111		325		330		335		
113	tat tgg gac gac ccg aag aag aga cca cta tta ctg caa tac gcg cgc					1056		
114	Tyr Trp Asp Asp Pro Lys Lys Arg Pro Leu Leu Leu Gln Tyr Ala Arg							
115		340		345		350		
117	gac gat gtc cgc gct act tac ggc tta gcc gag aag ata ttg ccg ttt					1104		
118	Asp Asp Val Arg Ala Thr Tyr Gly Leu Ala Glu Lys Ile Leu Pro Phe							
119		355		360		365		
121	gct atc cag ttg tcg tac gta aca ggt ctc cca cta gac cag gta ggt					1152		
122	Ala Ile Gln Leu Ser Tyr Val Thr Gly Leu Pro Leu Asp Gln Val Gly							
123		370		375		380		
125	gcg atg agt gtt ggc ttt cga ctt gaa tgg tac ctg ata cgc gcg gcg					1200		
126	Ala Met Ser Val Gly Phe Arg Leu Glu Trp Tyr Leu Ile Arg Ala Ala							
127	385		390		395	400		
129	ttt aag atg aaa gag ctt gtg ccg aac cgc gtt gag cgc cca gaa gag					1248		
130	Phe Lys Met Lys Glu Leu Val Pro Asn Arg Val Glu Arg Pro Glu Glu							
131		405		410		415		

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133	act	tac	cgt	ggc	gct	ata	gtt	ctt	gag	ccg	ttg	aga	ggc	gtg	cac	gag	1296
134	Thr	Tyr	Arg	Gly	Ala	Ile	Val	Leu	Glu	Pro	Leu	Arg	Gly	Val	His	Glu	
135				420					425					430			
137	aat	ata	gcc	gta	ctc	gac	ttt	agc	tgc	atg	tac	cca	aac	atc	atg	ata	1344
138	Asn	Ile	Ala	Val	Leu	Asp	Phe	Ser	Ser	Met	Tyr	Pro	Asn	Ile	Met	Ile	
139			435					440					445				
141	aag	tac	aat	gtt	ggt	cct	gac	acg	ctt	gtg	agg	cct	ggt	gaa	aag	tgt	1392
142	Lys	Tyr	Asn	Val	Gly	Pro	Asp	Thr	Leu	Val	Arg	Pro	Gly	Glu	Lys	Cys	
143		450					455					460					
145	ggc	gag	tgt	ggt	tgc	tgg	gag	gcc	ccg	gag	gtc	aag	cac	agg	ttc	cgt	1440
146	Gly	Glu	Cys	Gly	Cys	Trp	Glu	Ala	Pro	Glu	Val	Lys	His	Arg	Phe	Arg	
147	465					470					475					480	
149	agg	tgt	ccg	ccc	ggc	ttc	ttc	aag	aca	gtt	ctt	gag	agg	ctg	tta	gag	1488
150	Arg	Cys	Pro	Pro	Gly	Phe	Phe	Lys	Thr	Val	Leu	Glu	Arg	Leu	Leu	Glu	
151					485				490					495			
153	ctt	cgt	aag	cgt	gtg	cgt	gct	gaa	atg	aag	aag	tat	cct	ccg	gat	agc	1536
154	Leu	Arg	Lys	Arg	Val	Arg	Ala	Glu	Met	Lys	Lys	Tyr	Pro	Pro	Asp	Ser	
155			500					505					510				
157	cca	gaa	tat	cga	ctg	ttg	gat	gaa	agg	cag	aag	gcg	ttg	aag	gtt	ctt	1584
158	Pro	Glu	Tyr	Arg	Leu	Leu	Asp	Glu	Arg	Gln	Lys	Ala	Leu	Lys	Val	Leu	
159		515						520				525					
161	gca	aac	gct	agt	tac	ggc	tac	atg	ggt	tgg	agc	ggc	gct	agg	tgg	tat	1632
162	Ala	Asn	Ala	Ser	Tyr	Gly	Tyr	Met	Gly	Trp	Ser	Gly	Ala	Arg	Trp	Tyr	
163		530				535					540						
165	tgc	agg	gag	tgc	gca	aag	gct	gtc	acg	gct	tgg	ggt	agg	cac	ctc	ata	1680
166	Cys	Arg	Glu	Cys	Ala	Lys	Ala	Val	Thr	Ala	Trp	Gly	Arg	His	Leu	Ile	
167	545					550					555					560	
169	cgc	acc	gcc	atc	aac	ata	gct	cgt	aaa	cta	ggc	ctc	aag	gtg	atc	tac	1728
170	Arg	Thr	Ala	Ile	Asn	Ile	Ala	Arg	Lys	Leu	Gly	Leu	Lys	Val	Ile	Tyr	
171				565					570					575			
173	ggt	gac	aca	gat	tgc	ctc	ttc	gtg	acc	tat	gat	ccg	gag	aag	gtg	gaa	1776
174	Gly	Asp	Thr	Asp	Ser	Leu	Phe	Val	Thr	Tyr	Asp	Pro	Glu	Lys	Val	Glu	
175			580					585					590				
177	aat	ttc	atc	aaa	att	ata	aag	gag	gag	ctg	ggg	ttc	gaa	atc	aag	cta	1824
178	Asn	Phe	Ile	Lys	Ile	Ile	Lys	Glu	Glu	Leu	Gly	Phe	Glu	Ile	Lys	Leu	
179		595					600					605					
181	gag	aag	gtg	tac	aaa	cgc	tta	ttc	ttt	aca	gag	gct	aag	aag	agg	tac	1872
182	Glu	Lys	Val	Tyr	Lys	Arg	Leu	Phe	Phe	Thr	Glu	Ala	Lys	Lys	Arg	Tyr	
183		610					615					620					
185	gct	ggc	ctt	ctc	gag	gac	gga	cgt	ata	gat	att	gtc	ggt	ttc	gag	gct	1920
186	Ala	Gly	Leu	Leu	Glu	Asp	Gly	Arg	Ile	Asp	Ile	Val	Gly	Phe	Glu	Ala	
187	625					630					635					640	
189	gta	cgt	ggc	gat	tgg	tgt	gaa	ctc	gcc	aag	gag	gtt	cag	act	aag	gtt	1968
190	Val	Arg	Gly	Asp	Trp	Cys	Glu	Leu	Ala	Lys	Glu	Val	Gln	Thr	Lys	Val	
191				645					650						655		
193	gtc	gaa	ata	gta	ttg	aag	acg	agt	gag	gtg	aac	aag	gct	gta	gag	tac	2016
194	Val	Glu	Ile	Val	Leu	Lys	Thr	Ser	Glu	Val	Asn	Lys	Ala	Val	Glu	Tyr	
195			660						665					670			
197	gtc	agg	aag	att	gtg	aaa	gag	ttg	gag	gag	ggc	aag	gtt	ccc	ata	gag	2064

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198 Val Arg Lys Ile Val Lys Glu Leu Glu Glu Gly Lys Val Pro Ile Glu
199          675          680          685
201 aag ctt gta atc tgg aag acc ctt agt aag cgt ctt gag gag tac aca      2112
202 Lys Leu Val Ile Trp Lys Thr Leu Ser Lys Arg Leu Glu Glu Tyr Thr
203          690          695          700
205 acg gag gca cca cac gtc gtt gca gcg aag agg atg ctg tca gca ggc      2160
206 Thr Glu Ala Pro His Val Val Ala Ala Lys Arg Met Leu Ser Ala Gly
207 705          710          715          720
209 tac cgg gta agc cca ggc gac aag ata ggg tat gta ata gtg aag ggt      2208
210 Tyr Arg Val Ser Pro Gly Asp Lys Ile Gly Tyr Val Ile Val Lys Gly
211          725          730          735
213 ggt ggc cgt atc agt caa aga gca tgg cca tac ttc atg gtc aag gat      2256
214 Gly Gly Arg Ile Ser Gln Arg Ala Trp Pro Tyr Phe Met Val Lys Asp
215          740          745          750
217 cct agc cag ata gac gtg acc tac tat gtt gac cac caa atc atc ccg      2304
218 Pro Ser Gln Ile Asp Val Thr Tyr Tyr Val Asp His Gln Ile Ile Pro
219          755          760          765
221 gct gca ttg aga ata ctg ggc tac ttt ggc atc acc gag aag aag ctg      2352
222 Ala Ala Leu Arg Ile Leu Gly Tyr Phe Gly Ile Thr Glu Lys Lys Leu
223          770          775          780
225 aaa gca agt gca act ggg cag aag act ctc ttc gac ttt cta gcc aag      2400
226 Lys Ala Ser Ala Thr Gly Gln Lys Thr Leu Phe Asp Phe Leu Ala Lys
227 785          790          795          800
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230 Lys Ser Lys
234 <210> SEQ ID NO: 2
235 <211> LENGTH: 803
236 <212> TYPE: PRT
237 <213> ORGANISM: Pyrolobus fumarius
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246          20          25          30
249 Arg Val Val Leu Ile Asp Arg Ser Phe Arg Pro Tyr Phe Tyr Ala Leu
250          35          40          45
253 Leu Ala Pro Gly Ala Asp Pro Lys Gln Val Ala Gln Arg Ile Arg Ala
254          50          55          60
257 Leu Ser Arg Pro Lys Ser Pro Ile Ile Gly Val Glu Asp Asp Lys Arg
258 65          70          75          80
261 Lys Tyr Phe Gly Arg Pro Arg Arg Val Leu Arg Ile Arg Thr Val Leu
262          85          90          95
265 Pro Glu Ala Val Arg Glu Tyr Arg Glu Leu Val Lys Asn Val Asp Gly
266          100          105          110
269 Val Glu Asp Val Leu Glu Ala Asp Ile Arg Phe Ala Met Arg Tyr Leu
270          115          120          125
273 Ile Asp His Asp Leu Phe Pro Phe Thr Trp Tyr Arg Val Glu Ala Glu
274          130          135          140
277 Pro Leu Glu Asn Lys Met Gly Phe Arg Val Asp Lys Val Tyr Leu Val

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278 145          150          155          160
281 Lys Ser Arg Pro Glu Pro Leu Tyr Gly Glu Ala Leu Ala Pro Thr Lys
282          165          170          175
285 Leu Pro Asp Leu Arg Ile Leu Ala Phe Asp Ile Glu Val Tyr Ser Lys
286          180          185          190
289 Gln Gly Ser Pro Arg Pro Glu Arg Asp Pro Val Ile Val Ala Val
290          195          200          205
293 Lys Thr Asp Asp Gly Asp Glu Val Leu Phe Ile Ala Glu Gly Lys Asp
294          210          215          220
297 Asp Arg Lys Pro Ile Arg Glu Phe Val Glu Tyr Val Lys Arg Tyr Asp
298 225          230          235          240
301 Pro Asp Ile Ile Val Gly Tyr Asn Asn Asn His Phe Asp Trp Pro Tyr
302          245          250          255
305 Leu Leu Arg Arg Ala Arg Ile Leu Gly Ile Lys Leu Asp Val Thr Arg
306          260          265          270
309 Arg Val Gly Ala Glu Pro Thr Thr Ser Val His Gly His Val Ser Val
310          275          280          285
313 Pro Gly Arg Leu Asn Val Asp Leu Tyr Asp Tyr Ala Glu Glu Met Pro
314          290          295          300
317 Glu Ile Lys Ile Lys Ser Leu Glu Glu Val Ala Glu Tyr Leu Gly Val
318 305          310          315          320
321 Met Lys Lys Ser Glu Arg Val Ile Ile Asn Trp Trp Glu Ile Pro Asp
322          325          330          335
325 Tyr Trp Asp Asp Pro Lys Lys Arg Pro Leu Leu Leu Gln Tyr Ala Arg
326          340          345          350
329 Asp Asp Val Arg Ala Thr Tyr Gly Leu Ala Glu Lys Ile Leu Pro Phe
330          355          360          365
333 Ala Ile Gln Leu Ser Tyr Val Thr Gly Leu Pro Leu Asp Gln Val Gly
334          370          375          380
337 Ala Met Ser Val Gly Phe Arg Leu Glu Trp Tyr Leu Ile Arg Ala Ala
338 385          390          395          400
341 Phe Lys Met Lys Glu Leu Val Pro Asn Arg Val Glu Arg Pro Glu Glu
342          405          410          415
345 Thr Tyr Arg Gly Ala Ile Val Leu Glu Pro Leu Arg Gly Val His Glu
346          420          425          430
349 Asn Ile Ala Val Leu Asp Phe Ser Ser Met Tyr Pro Asn Ile Met Ile
350          435          440          445
353 Lys Tyr Asn Val Gly Pro Asp Thr Leu Val Arg Pro Gly Glu Lys Cys
354          450          455          460
357 Gly Glu Cys Gly Cys Trp Glu Ala Pro Glu Val Lys His Arg Phe Arg
358 465          470          475          480
361 Arg Cys Pro Pro Gly Phe Phe Lys Thr Val Leu Glu Arg Leu Leu Glu
362          485          490          495
365 Leu Arg Lys Arg Val Arg Ala Glu Met Lys Lys Tyr Pro Pro Asp Ser
366          500          505          510
369 Pro Glu Tyr Arg Leu Leu Asp Glu Arg Gln Lys Ala Leu Lys Val Leu
370          515          520          525
373 Ala Asn Ala Ser Tyr Gly Tyr Met Gly Trp Ser Gly Ala Arg Trp Tyr
374          530          535          540

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VERIFICATION SUMMARY

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